

Exhibit B
SEQ ID NO 1 versus human genomic sequence

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
33,840 sequences; 200,810,911,373 total letters

Query= LEX143seqid1
(1311 letters)

	Score
E	
Sequences producing significant alignments:	(bits)
Value	

AL121673.41.1.151163	<u>392</u>
e-106	

>AL121673.41.1.151163
Length = 151163

Score = 392 bits (198), Expect = e-106
Identities = 201/202 (99%)
Strand = Plus / Plus

Query: 57 caggccccgagtgccaggcatggacggggacgctgctgctgggcacgtgccttctgtactg
116

Sbjct: 17379 caggccccgagtgccaggcatggacggggacgctgctgctgggcacatgccttctgtactg
17438

Query: 117 cgccccgctccagcatgcccattctgcaccgtctccatgagccaggacttcggctggaacaa
176

Sbjct: 17439 cgccccgctccagcatgcccattctgcaccgtctccatgagccaggacttcggctggaacaa
17498

Query: 177 gaaggaggccggcatcgtgctcagcagcttcttctggggctactgcctgacacaggttgt
236

Sbjct: 17499 gaaggaggccggcatcgtgctcagcagcttcttctggggctactgcctgacacaggttgt
17558

Query: 237 gggcggccacctcggggatcgg 258

Sbjct: 17559 gggcggccacctcggggatcgg 17580

Score = 335 bits (169), Expect = 4e-89
Identities = 169/169 (100%)
Strand = Plus / Plus

Query: 1143 ggcagggtgtcgtgggtgtgtgtctagggcggtacttgatggagaccacgggctcctggac
1202

Sbjct: 27949 ggcagggtgtcgtgggtgtgtgtctagggcggtacttgatggagaccacgggctcctggac
28008

Query: 1203 ttgcctgttcaaccttgtggccatcatcagcaacctggggctgtgcaccttcctggtgtt
1262

Sbjct: 28009 ttgcctgttcaaccttgtggccatcatcagcaacctggggctgtgcaccttcctggtgtt
28068

Query: 1263 tggacaggctcagaggggtggacctgagctctacccatgaggacctctag 1311

Sbjct: 28069 tggacaggctcagaggggtggacctgagctctacccatgaggacctctag 28117

Score = 281 bits (142), Expect = 5e-73
Identities = 142/142 (100%)
Strand = Plus / Plus

Query: 257 ggattgggggtgagaagggtcatcctgctgtcagcctctgcctggggctccatcacggccg
316

Sbjct: 18057 ggattgggggtgagaagggtcatcctgctgtcagcctctgcctggggctccatcacggccg
18116

Query: 317 tcacccactgctcgcccacctgagcagtgcccacctggccttcacgttctcagca
376

Sbjct: 18117 tcacccactgctcgcccacctgagcagtgcccacctggccttcacgttctcagca
18176

Query: 377 tcctcatgggcttgctccaagg 398

Sbjct: 18177 tcctcatgggcttgctccaagg 18198

Score = 262 bits (132), Expect = 5e-67
Identities = 132/132 (100%)
Strand = Plus / Plus

Query: 497 ggacgctgctgaccggggcggtgggctccctgctcctggaatggtacggctggcagagca
556

Sbjct: 23240 ggacgctgctgaccggggcggtgggctccctgctcctggaatggtacggctggcagagca
23299

Query: 557 tcttctatttctccggcgccctcaccttgctttgggtgtggtacgtgtacaggtacctgc
616

Sbjct: 23300 tcttctatttctccggcgccctcaccttgctttgggtgtggtacgtgtacaggtacctgc
23359

Query: 617 tgagtgaagaaag 628

Sbjct: 23360 tgagtgaagaaag 23371

Score = 240 bits (121), Expect = 2e-60
Identities = 121/121 (100%)
Strand = Plus / Plus

Query: 941 tgcagggcatgggccttggcctctccagcgtctttgctctgtgcctggggccacacctcca
1000

Sbjct: 26222 tgcagggcatgggccttggcctctccagcgtctttgctctgtgcctggggccacacctcca
26281

Query: 1001 gcttctgtgagtcgtgtggtctttgcatcagcctccatcggcctccagaccttcaaccaca
1060

Sbjct: 26282 gcttctgtgagtcgtgtggtctttgcatcagcctccatcggcctccagaccttcaaccaca
26341

Query: 1061 g 1061

Sbjct: 26342 g 26342

Score = 204 bits (103), Expect = 1e-49
Identities = 103/103 (100%)
Strand = Plus / Plus

Query: 396 aggggtttacttccctgccctgaccagcctgctgtcgcagaaggtgcgggagagtgcgcg
455

Sbjct: 21119 aggggtttacttccctgccctgaccagcctgctgtcgcagaaggtgcgggagagtgcgcg
21178

Query: 456 agccttcacctacagcatcgtgggcgcggctcccagtttggg 498

Sbjct: 21179 agccttcacctacagcatcgtgggcgcggctcccagtttggg 21221

Score = 196 bits (99), Expect = 2e-47
Identities = 99/99 (100%)
Strand = Plus / Plus

Query: 725 gggcagccgctcgtctcccagctctctgcagcctgctccttcttcatcctcctctcctggc
784
|||||
Sbjct: 24200 gggcagccgctcgtctcccagctctctgcagcctgctccttcttcatcctcctctcctggc
24259

Query: 785 tgccaccttcttcgaggagaccttccccgacgccaagg 823
|||||
Sbjct: 24260 tgccaccttcttcgaggagaccttccccgacgccaagg 24298

Score = 190 bits (96), Expect = 2e-45
Identities = 99/100 (99%)
Strand = Plus / Plus

Query: 627 agatctcatcctggccttgggtgtcctggcccaaagccggccggtgtccaggcacagcag
686
|||||
Sbjct: 23888 agatctcatcctggccttgggtgtcctggcccaaagccggccggtgtccaggcacaacag
23947

Query: 687 agtcccctggagacggctcttccggaagcctgctgtctgg 726
|||||
Sbjct: 23948 agtcccctggagacggctcttccggaagcctgctgtctgg 23987

Score = 182 bits (92), Expect = 4e-43
Identities = 92/92 (100%)
Strand = Plus / Plus

Query: 821 agggctggatcttcaacgtggttccttgggtggcgattccggccagtctattcagcg
880
|||||
Sbjct: 24843 agggctggatcttcaacgtggttccttgggtggcgattccggccagtctattcagcg
24902

Query: 881 ggtttctctctgatcatctcatcaatcagggt 912
|||||
Sbjct: 24903 ggtttctctctgatcatctcatcaatcagggt 24934

Score = 129 bits (65), Expect = 5e-27
Identities = 65/65 (100%)
Strand = Plus / Plus

Query: 1056 ccacagtggcatttctgttaacatccaggacttggccccgtcctgcgccggctttctgtt
1115
|||||
Sbjct: 27136 ccacagtggcatttctgttaacatccaggacttggccccgtcctgcgccggctttctgtt
27195

Query: 1116 tgggtg 1120
|||||
Sbjct: 27196 tgggtg 27200

Score = 113 bits (57), Expect = 3e-22
Identities = 57/57 (100%)
Strand = Plus / Plus

Query: 1 atgcagccacccccagacgaggcccgagggacatggccggggacacccagtgggtcc 57
|||||
Sbjct: 13448 atgcagccacccccagacgaggcccgagggacatggccggggacacccagtgggtcc
13504

Score = 73.8 bits (37), Expect = 2e-10
Identities = 37/37 (100%)
Strand = Plus / Plus

Query: 910 ggttacagagccatcacggtgcggaagctcatgcagg 946
|||||
Sbjct: 25748 ggttacagagccatcacggtgcggaagctcatgcagg 25784

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 1117 ggtgtggccaacacagccggggccttggcaggtg 1150
|||||
Sbjct: 27319 ggtgtggccaacacagccggggccttggcaggtg 27352

Database: Homo_sapiens.latestgp.masked.fa
Posted date: May 12, 2003 5:02 PM
Number of letters in database: 200,810,911,373
Number of sequences in database: 33,840

Lambda	K	H
1.37	0.711	1.31

Gapped Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
Number of Hits to DB: 0
length of query: 2624
length of database: 200,810,911,373
effective HSP length: 22
effective length of query: 1289

effective search space used: 0

T: 0

A: 0

X1: 0 (0.0 bits)

X2: 20 (39.6 bits)

S1: 12 (24.3 bits)

S2: 23 (46.1 bits)